

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/024,623

DATE: 01/16/2002
TIME: 18:29:15

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\01162002\J024623.raw

3 <110> APPLICANT: Curtis, Rory A.J.
5 <120> TITLE OF INVENTION: 8099, 46455, 54414, 53763, 67076, 67102, 44181,
6 67084FL, AND 67084 ALT, HUMAN PROTEINS AND METHODS OF
7 USE THEREOF
9 <130> FILE REFERENCE: MNI-214CP
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/024,623
C--> 11 <141> CURRENT FILING DATE: 2001-12-17
11 <150> PRIOR APPLICATION NUMBER: US 60/256,240
12 <151> PRIOR FILING DATE: 2000-12-15
14 <150> PRIOR APPLICATION NUMBER: US 60/256,588
15 <151> PRIOR FILING DATE: 2000-12-18
17 <150> PRIOR APPLICATION NUMBER: US 60/258,028
18 <151> PRIOR FILING DATE: 2000-12-21
20 <160> NUMBER OF SEQ ID NOS: 40
22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 2725
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (180)...(2033)
33 <400> SEQUENCE: 1
34 ccacgcgtcc ggccttccga aatagaaaca aagttggtca caaatcacat tagctttgcc 60
35 cgaagttttt cccacactc ttcttttagca tgctattatg gggaaagtga ccactcctgg 120
36 gagcgggggt ggtcggggcg gtttggtggc ggggaagcgg ctgtaacttc tacgtgacc 179
37 atg gta cct gtt gaa aac acc gag ggc ccc agt ctg ctg aac cag aag 227
38 Met Val Pro Val Glu Asn Thr Glu Gly Pro Ser Leu Leu Asn Gln Lys
39 1 5 10 15
41 ggg aca gcc gtg gag acg gag ggc agc ggc agc cgg cat cct ccc tgg 275
42 Gly Thr Ala Val Glu Thr Glu Gly Ser Gly Ser Arg His Pro Pro Trp
43 20 25 30
45 gcg aga ggc tgc ggc atg ttt acc ttc ctg tca tct gtc act gct gct 323
46 Ala Arg Gly Cys Gly Met Phe Thr Phe Leu Ser Ser Val Thr Ala Ala
47 35 40 45
49 gtc agt ggc ctc ctg gtg ggt tat gaa ctt ggg atc atc tct ggg gct 371
50 Val Ser Gly Leu Leu Val Gly Tyr Glu Leu Gly Ile Ile Ser Gly Ala
51 50 55 60
53 ctt ctt cag atc aaa acc tta tta gcc ctg agc tgc cat gag cag gaa 419
54 Leu Leu Gln Ile Lys Thr Leu Leu Ala Leu Ser Cys His Glu Gln Glu
55 65 70 75 80
57 atg gtt gtg agc tcc ctc gtc att gga gcc ctc ctt gcc tca ctc acc 467
58 Met Val Val Ser Ser Leu Val Ile Gly Ala Leu Leu Ala Ser Leu Thr
59 85 90 95
61 gga ggg gtc ctg ata gac aga tat gga aga agg aca gca atc atc ttg 515
62 Gly Gly Val Leu Ile Asp Arg Tyr Gly Arg Arg Thr Ala Ile Ile Leu
63 100 105 110

ENTERED

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65 tca tcc tgc ctg ctt gga ctc gga agc tta gtc ttg atc ctc agt tta 563
66 Ser Ser Cys Leu Leu Gly Leu Gly Ser Leu Val Leu Ile Leu Ser Leu
67      115      120      125
69 tcc tac acg gtt ctt ata gtg gga cgc att gcc ata ggg gtc tcc atc 611
70 Ser Tyr Thr Val Leu Ile Val Gly Arg Ile Ala Ile Gly Val Ser Ile
71      130      135      140
73 tcc ctc tct tcc att gcc act tgt gtt tac atc gca gag att gct cct 659
74 Ser Leu Ser Ser Ile Ala Thr Cys Val Tyr Ile Ala Glu Ile Ala Pro
75 145      150      155      160
77 caa cac aga aga ggc ctt ctt gtg tca ctg aat gag ctg atg att gtc 707
78 Gln His Arg Arg Gly Leu Leu Val Ser Leu Asn Glu Leu Met Ile Val
79      165      170      175
81 atc ggc att ctt tct gcc tat att tca aat tac gca ttt gcc aat gtt 755
82 Ile Gly Ile Leu Ser Ala Tyr Ile Ser Asn Tyr Ala Phe Ala Asn Val
83      180      185      190
85 ttc cat ggc tgg aag tac atg ttt ggt ctt gtg att ccc ttg gga gtt 803
86 Phe His Gly Trp Lys Tyr Met Phe Gly Leu Val Ile Pro Leu Gly Val
87      195      200      205
89 ttg caa gca att gca atg tat ttt ctt cct cca agc cct cgg ttt ctg 851
90 Leu Gln Ala Ile Ala Met Tyr Phe Leu Pro Pro Ser Pro Arg Phe Leu
91      210      215      220
93 gtg atg aaa gga caa gag gga gct gct agc aag gtt ctt gga agg tta 899
94 Val Met Lys Gly Gln Glu Gly Ala Ala Ser Lys Val Leu Gly Arg Leu
95 225      230      235      240
97 aga gca ctc tca gat aca act gag gaa ctc act gtg atc aaa tcc tcc 947
98 Arg Ala Leu Ser Asp Thr Thr Glu Glu Leu Thr Val Ile Lys Ser Ser
99      245      250      255
101 ctg aaa gat gaa tat cag tac agt ttt tgg gat ctg ttt cgt tca aaa 995
102 Leu Lys Asp Glu Tyr Gln Tyr Ser Phe Trp Asp Leu Phe Arg Ser Lys
103      260      265      270
105 gac aac atg cgg acc cga ata atg ata gga cta aca cta gta ttt ttt 1043
106 Asp Asn Met Arg Thr Arg Ile Met Ile Gly Leu Thr Leu Val Phe Phe
107      275      280      285
109 gta caa atc act ggc caa cca aac ata ttg ttc tat gca tca act gtt 1091
110 Val Gln Ile Thr Gly Gln Pro Asn Ile Leu Phe Tyr Ala Ser Thr Val
111      290      295      300
113 ttg aag tca gtt gga ttt caa agc aat gag gca gct agc ctc gcc tcc 1139
114 Leu Lys Ser Val Gly Phe Gln Ser Asn Glu Ala Ala Ser Leu Ala Ser
115 305      310      315      320
117 act ggg gtt gga gtc gtc aag gtc att agc acc atc cct gcc act ctt 1187
118 Thr Gly Val Gly Val Val Lys Val Ile Ser Thr Ile Pro Ala Thr Leu
119      325      330      335
121 ctt gta gac cat gtc ggc agc aaa aca ttc ctc tgc att ggc tcc tct 1235
122 Leu Val Asp His Val Gly Ser Lys Thr Phe Leu Cys Ile Gly Ser Ser
123      340      345      350
125 gtg atg gca gct tgc ttg gtg acc atg ggc atc gta aat ctc aac atc 1283
126 Val Met Ala Ala Ser Leu Val Thr Met Gly Ile Val Asn Leu Asn Ile
127      355      360      365
129 cac atg aac ttc acc cat atc tgc aga agc cac aat tct atc aac cag 1331

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130 His Met Asn Phe Thr His Ile Cys Arg Ser His Asn Ser Ile Asn Gln
131      370      375      380
133 tcc ttg gat gag tct gtg att tat gga cca gga aac ctg tca acc aac 1379
134 Ser Leu Asp Glu Ser Val Ile Tyr Gly Pro Gly Asn Leu Ser Thr Asn
135 385      390      395      400
137 aac aat act ctc aga gac cac ttc aaa ggg att tct tcc cat agc aga 1427
138 Asn Asn Thr Leu Arg Asp His Phe Lys Gly Ile Ser Ser His Ser Arg
139      405      410      415
141 agc tca ctc atg ccc ctg aga aat gat gtg gat aag aga ggg gag acg 1475
142 Ser Ser Leu Met Pro Leu Arg Asn Asp Val Asp Lys Arg Gly Glu Thr
143      420      425      430
145 acc tca gca tcc ttg cta aat gct gga tta agc cac act gaa tac cag 1523
146 Thr Ser Ala Ser Leu Leu Asn Ala Gly Leu Ser His Thr Glu Tyr Gln
147      435      440      445
149 ata gtc aca gac cct ggg gac gtc cca gct ttt ttg aaa tgg ctg tcc 1571
150 Ile Val Thr Asp Pro Gly Asp Val Pro Ala Phe Leu Lys Trp Leu Ser
151      450      455      460
153 tta gcc agc ttg ctt gtt tat gtt gct gct ttt tca att ggt cta gga 1619
154 Leu Ala Ser Leu Leu Val Tyr Val Ala Ala Phe Ser Ile Gly Leu Gly
155 465      470      475      480
157 cca atg ccc tgg ctg gtg ctc agc gag atc ttt cct ggt ggg atc aga 1667
158 Pro Met Pro Trp Leu Val Leu Ser Glu Ile Phe Pro Gly Gly Ile Arg
159      485      490      495
161 gga cga gcc atg gct tta act tct agc atg aac tgg ggc atc aat ctc 1715
162 Gly Arg Ala Met Ala Leu Thr Ser Ser Met Asn Trp Gly Ile Asn Leu
163      500      505      510
165 ctc atc tcg ctg aca ttt ttg act gta act gat ctt att ggc ctg cca 1763
166 Leu Ile Ser Leu Thr Phe Leu Thr Val Thr Asp Leu Ile Gly Leu Pro
167      515      520      525
169 tgg gtg tgc ttt ata tat aca atc atg agt cta gca tcc ctg ctt ttt 1811
170 Trp Val Cys Phe Ile Tyr Thr Ile Met Ser Leu Ala Ser Leu Leu Phe
171      530      535      540
173 gtt gtt atg ttt ata cct gag aca aag gga tgc tct ttg gaa caa ata 1859
174 Val Val Met Phe Ile Pro Glu Thr Lys Gly Cys Ser Leu Glu Gln Ile
175 545      550      555      560
177 tca atg gag cta gca aaa gtg aac tat gtg aaa aac aac att tgt ttt 1907
178 Ser Met Glu Leu Ala Lys Val Asn Tyr Val Lys Asn Asn Ile Cys Phe
179      565      570      575
181 atg agt cat cac caa gaa gaa tta gtg cca aaa cag cct caa aaa aga 1955
182 Met Ser His His Gln Glu Glu Leu Val Pro Lys Gln Pro Gln Lys Arg
183      580      585      590
185 aaa ccc cag gag cag ctc ttg gag tgt aac aag ctg tgt ggt agg ggc 2003
186 Lys Pro Gln Glu Gln Leu Leu Glu Cys Asn Lys Leu Cys Gly Arg Gly
187      595      600      605
189 caa tcc agg cag ctt tct cca gag acc taa tggcctcaac accttctgaa 2053
190 Gln Ser Arg Gln Leu Ser Pro Glu Thr *
191      610      615
193 cgtggatagt gccagaacac ttaggagggt gtctttggac caatgcatag ttgcgactcc 2113
194 tgtgctctct tttcagtgct atggaactgg ttttgaagag acactctgaa atgataaaga 2173

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195 cagcctttaa tccccctcct cccagaagg aacctcaaaa ggtagatgag gtacaaggct 2233
196 ctaagtgatc tctttttctg agcaggatat cagggttaaaa aaaaaaagtt actggctggg 2293
197 ttaatacttt ctaccttctt cacagagcag cctttgaata gactatgtcc tagtgaagac 2353
198 atcaacctcc gccttaagct atgtatgtat ggaggccagt cgcagcttta ttatgcagac 2413
199 acacaagtgg tctggacatg aggggtacagt ttctgcctac caagacacta cttgcactgg 2473
200 atcttacgca aaaaagaacc agaacacaca gtgtggacaa ctgcccataat attctatcta 2533
201 gattaggaga gggctcctggc taggatttta gtggtaatc ctagttacat tcaacaagta 2593
202 taaagattat agagcttatt ttatgaacta taaactataa tttaatgcaa aatatccttt 2653
203 tatgaatttc atgttaatat tgtgaaatat taaaataatt ccgcaataaa aaaaaaaaaa 2713
204 aagggcggcc gc 2725
206 <210> SEQ ID NO: 2
207 <211> LENGTH: 617
208 <212> TYPE: PRT
209 <213> ORGANISM: Homo sapiens
211 <400> SEQUENCE: 2
212 Met Val Pro Val Glu Asn Thr Glu Gly Pro Ser Leu Leu Asn Gln Lys
213 1 5 10 15
214 Gly Thr Ala Val Glu Thr Glu Gly Ser Gly Ser Arg His Pro Pro Trp
215 20 25 30
216 Ala Arg Gly Cys Gly Met Phe Thr Phe Leu Ser Ser Val Thr Ala Ala
217 35 40 45
218 Val Ser Gly Leu Leu Val Gly Tyr Glu Leu Gly Ile Ile Ser Gly Ala
219 50 55 60
220 Leu Leu Gln Ile Lys Thr Leu Leu Ala Leu Ser Cys His Glu Gln Glu
221 65 70 75 80
222 Met Val Val Ser Ser Leu Val Ile Gly Ala Leu Leu Ala Ser Leu Thr
223 85 90 95
224 Gly Gly Val Leu Ile Asp Arg Tyr Gly Arg Arg Thr Ala Ile Ile Leu
225 100 105 110
226 Ser Ser Cys Leu Leu Gly Leu Gly Ser Leu Val Leu Ile Leu Ser Leu
227 115 120 125
228 Ser Tyr Thr Val Leu Ile Val Gly Arg Ile Ala Ile Gly Val Ser Ile
229 130 135 140
230 Ser Leu Ser Ser Ile Ala Thr Cys Val Tyr Ile Ala Glu Ile Ala Pro
231 145 150 155 160
232 Gln His Arg Arg Gly Leu Leu Val Ser Leu Asn Glu Leu Met Ile Val
233 165 170 175
234 Ile Gly Ile Leu Ser Ala Tyr Ile Ser Asn Tyr Ala Phe Ala Asn Val
235 180 185 190
236 Phe His Gly Trp Lys Tyr Met Phe Gly Leu Val Ile Pro Leu Gly Val
237 195 200 205
238 Leu Gln Ala Ile Ala Met Tyr Phe Leu Pro Pro Ser Pro Arg Phe Leu
239 210 215 220
240 Val Met Lys Gly Gln Glu Gly Ala Ala Ser Lys Val Leu Gly Arg Leu
241 225 230 235 240
242 Arg Ala Leu Ser Asp Thr Thr Glu Glu Leu Thr Val Ile Lys Ser Ser
243 245 250 255
244 Leu Lys Asp Glu Tyr Gln Tyr Ser Phe Trp Asp Leu Phe Arg Ser Lys
245 260 265 270

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246 Asp Asn Met Arg Thr Arg Ile Met Ile Gly Leu Thr Leu Val Phe Phe
247           275           280           285
248 Val Gln Ile Thr Gly Gln Pro Asn Ile Leu Phe Tyr Ala Ser Thr Val
249           290           295           300
250 Leu Lys Ser Val Gly Phe Gln Ser Asn Glu Ala Ala Ser Leu Ala Ser
251 305           310           315           320
252 Thr Gly Val Gly Val Val Lys Val Ile Ser Thr Ile Pro Ala Thr Leu
253           325           330           335
254 Leu Val Asp His Val Gly Ser Lys Thr Phe Leu Cys Ile Gly Ser Ser
255           340           345           350
256 Val Met Ala Ala Ser Leu Val Thr Met Gly Ile Val Asn Leu Asn Ile
257           355           360           365
258 His Met Asn Phe Thr His Ile Cys Arg Ser His Asn Ser Ile Asn Gln
259           370           375           380
260 Ser Leu Asp Glu Ser Val Ile Tyr Gly Pro Gly Asn Leu Ser Thr Asn
261 385           390           395           400
262 Asn Asn Thr Leu Arg Asp His Phe Lys Gly Ile Ser Ser His Ser Arg
263           405           410           415
264 Ser Ser Leu Met Pro Leu Arg Asn Asp Val Asp Lys Arg Gly Glu Thr
265           420           425           430
266 Thr Ser Ala Ser Leu Leu Asn Ala Gly Leu Ser His Thr Glu Tyr Gln
267           435           440           445
268 Ile Val Thr Asp Pro Gly Asp Val Pro Ala Phe Leu Lys Trp Leu Ser
269           450           455           460
270 Leu Ala Ser Leu Leu Val Tyr Val Ala Ala Phe Ser Ile Gly Leu Gly
271 465           470           475           480
272 Pro Met Pro Trp Leu Val Leu Ser Glu Ile Phe Pro Gly Gly Ile Arg
273           485           490           495
274 Gly Arg Ala Met Ala Leu Thr Ser Ser Met Asn Trp Gly Ile Asn Leu
275           500           505           510
276 Leu Ile Ser Leu Thr Phe Leu Thr Val Thr Asp Leu Ile Gly Leu Pro
277           515           520           525
278 Trp Val Cys Phe Ile Tyr Thr Ile Met Ser Leu Ala Ser Leu Leu Phe
279           530           535           540
280 Val Val Met Phe Ile Pro Glu Thr Lys Gly Cys Ser Leu Glu Gln Ile
281 545           550           555           560
282 Ser Met Glu Leu Ala Lys Val Asn Tyr Val Lys Asn Asn Ile Cys Phe
283           565           570           575
284 Met Ser His His Gln Glu Glu Leu Val Pro Lys Gln Pro Gln Lys Arg
285           580           585           590
286 Lys Pro Gln Glu Gln Leu Leu Glu Cys Asn Lys Leu Cys Gly Arg Gly
287           595           600           605
288 Gln Ser Arg Gln Leu Ser Pro Glu Thr
289           610           615
292 <210> SEQ ID NO: 3
293 <211> LENGTH: 1854
294 <212> TYPE: DNA
295 <213> ORGANISM: Homo sapiens
297 <220> FEATURE:

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→ Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1152 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:7449 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36
L:7473 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36
L:7533 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:7566 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38
L:7599 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39
L:7622 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40